

Fig. 2A

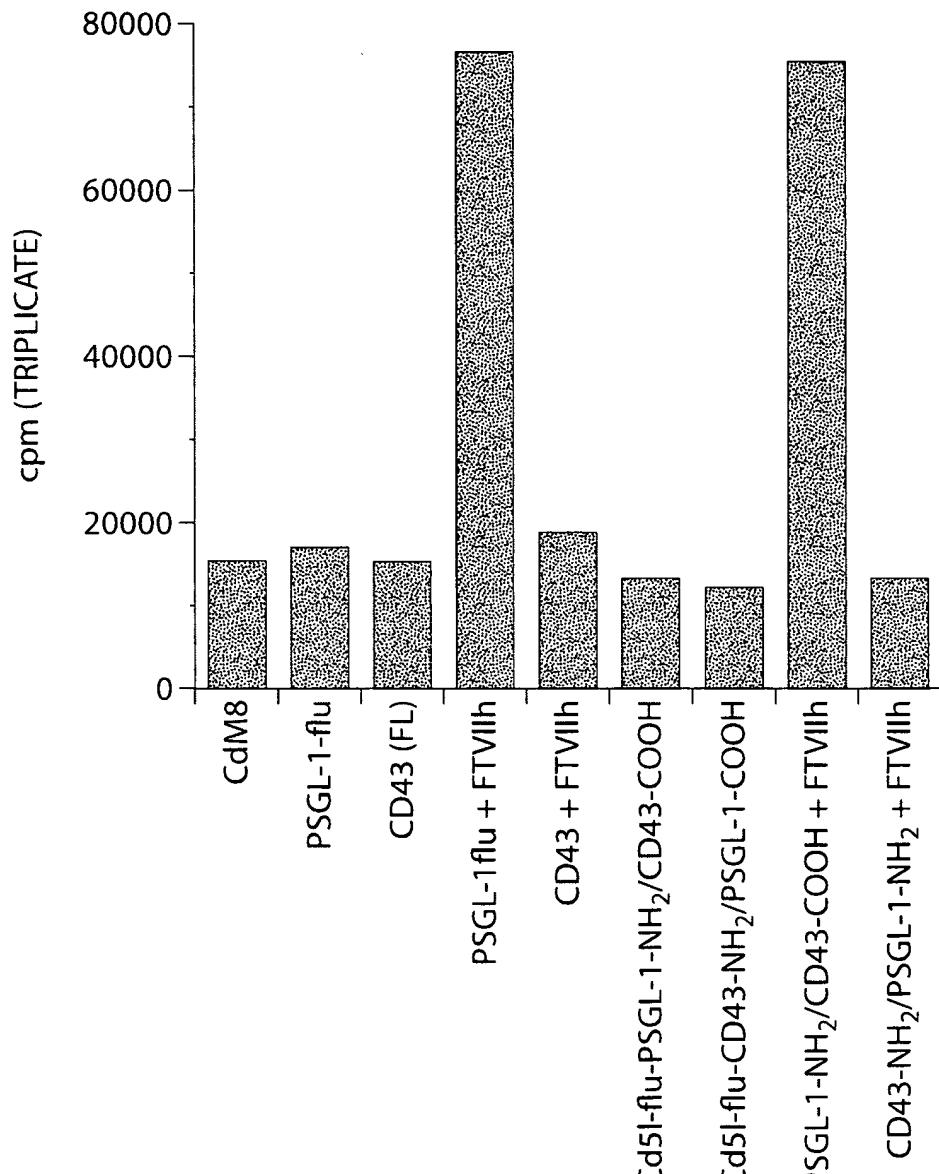
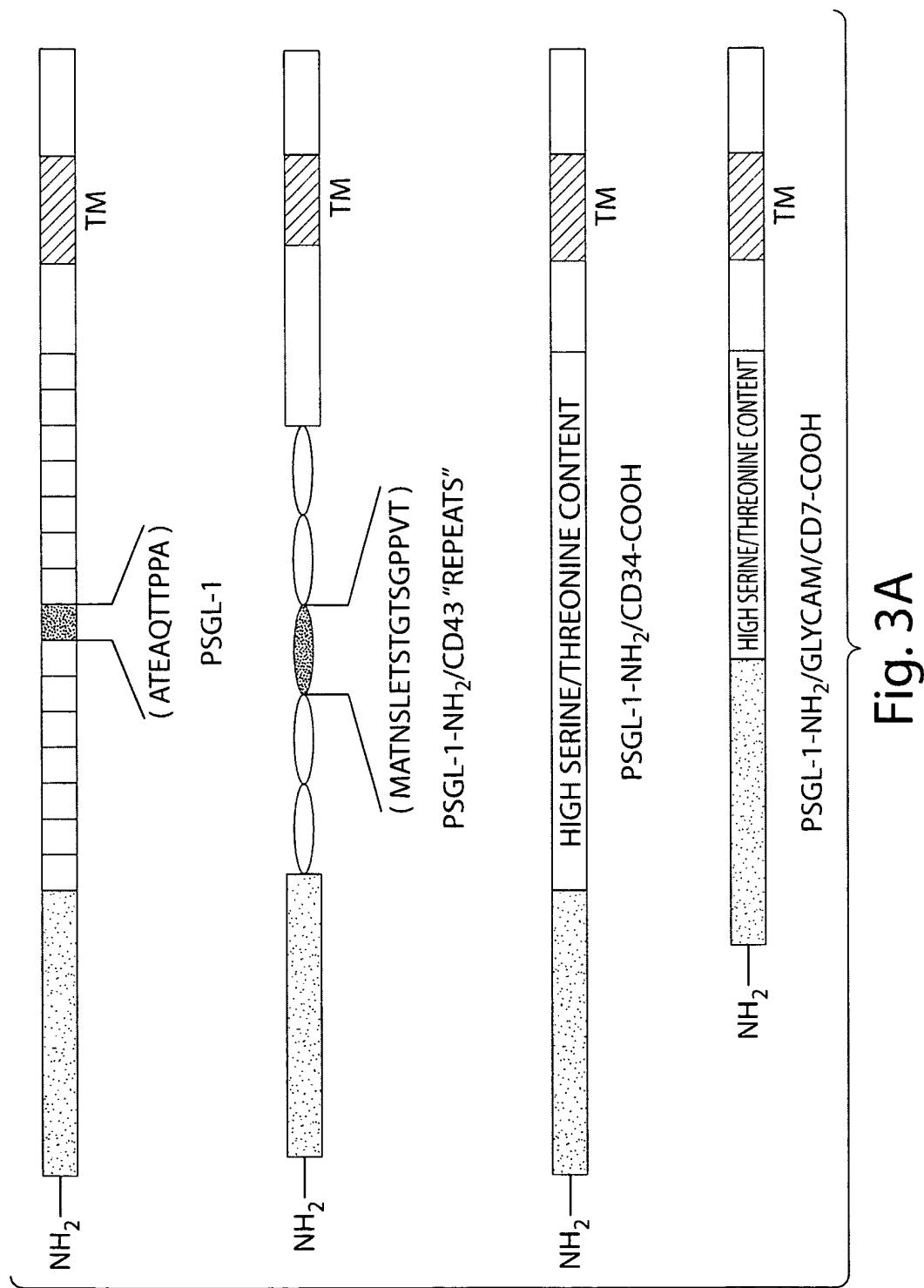


Fig. 2B



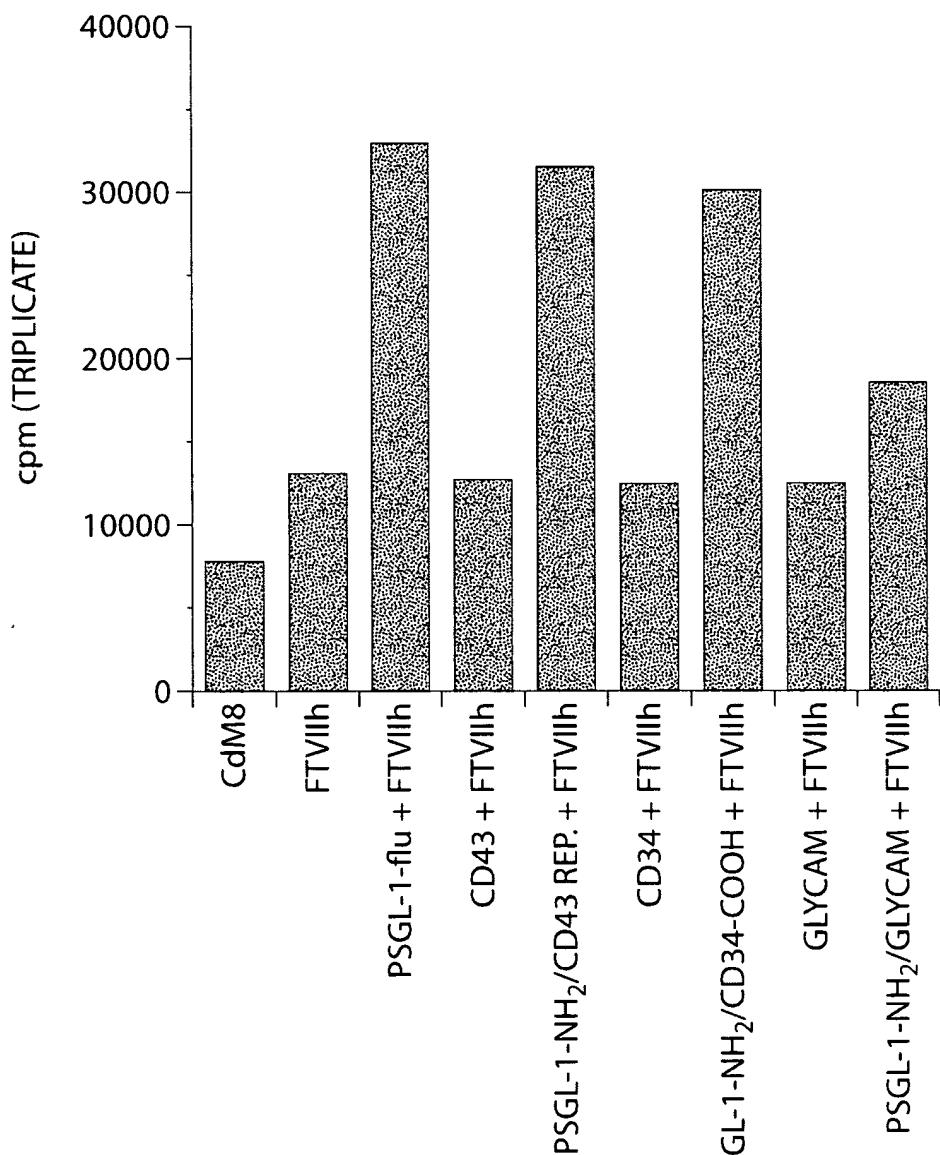
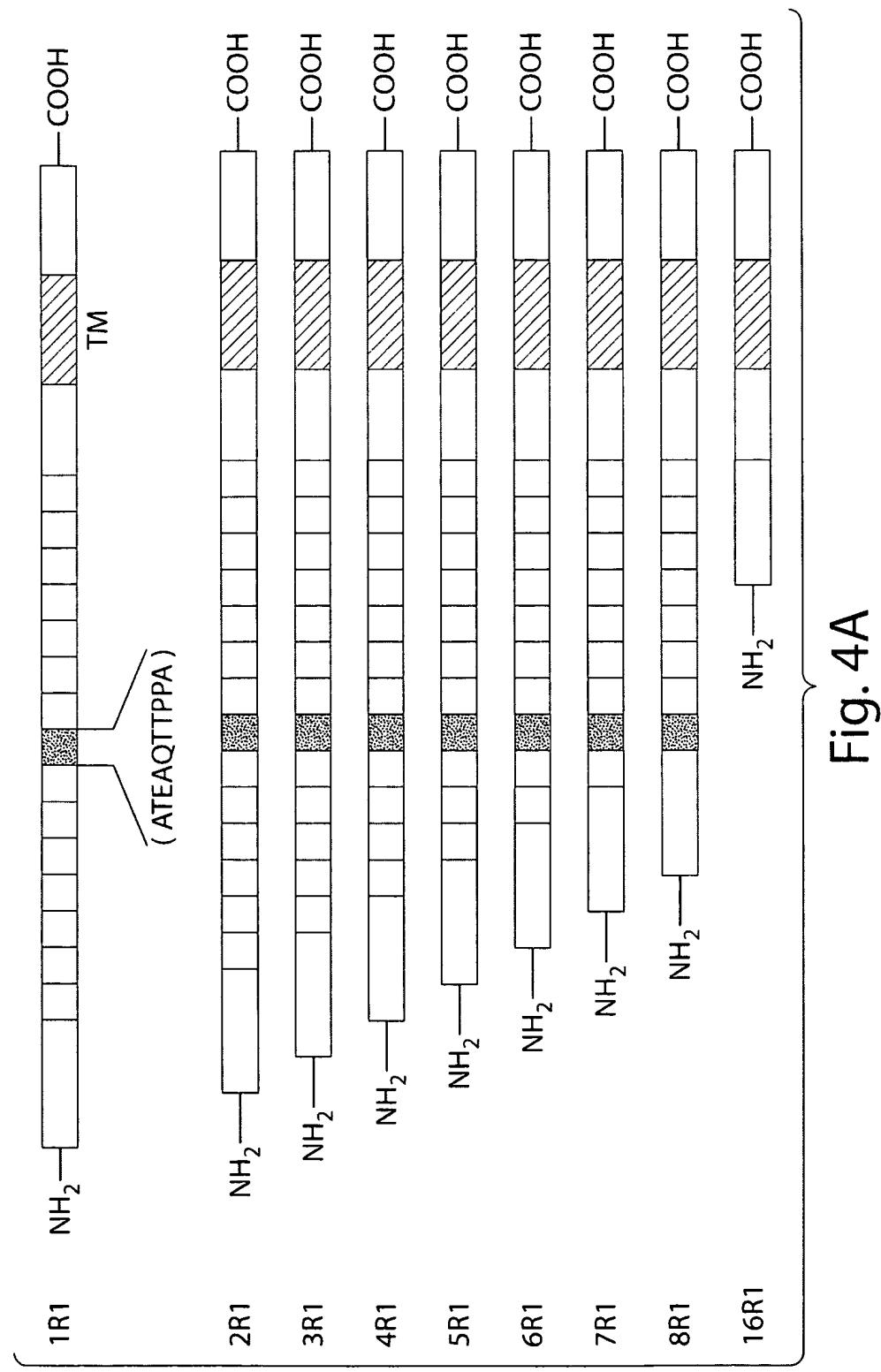
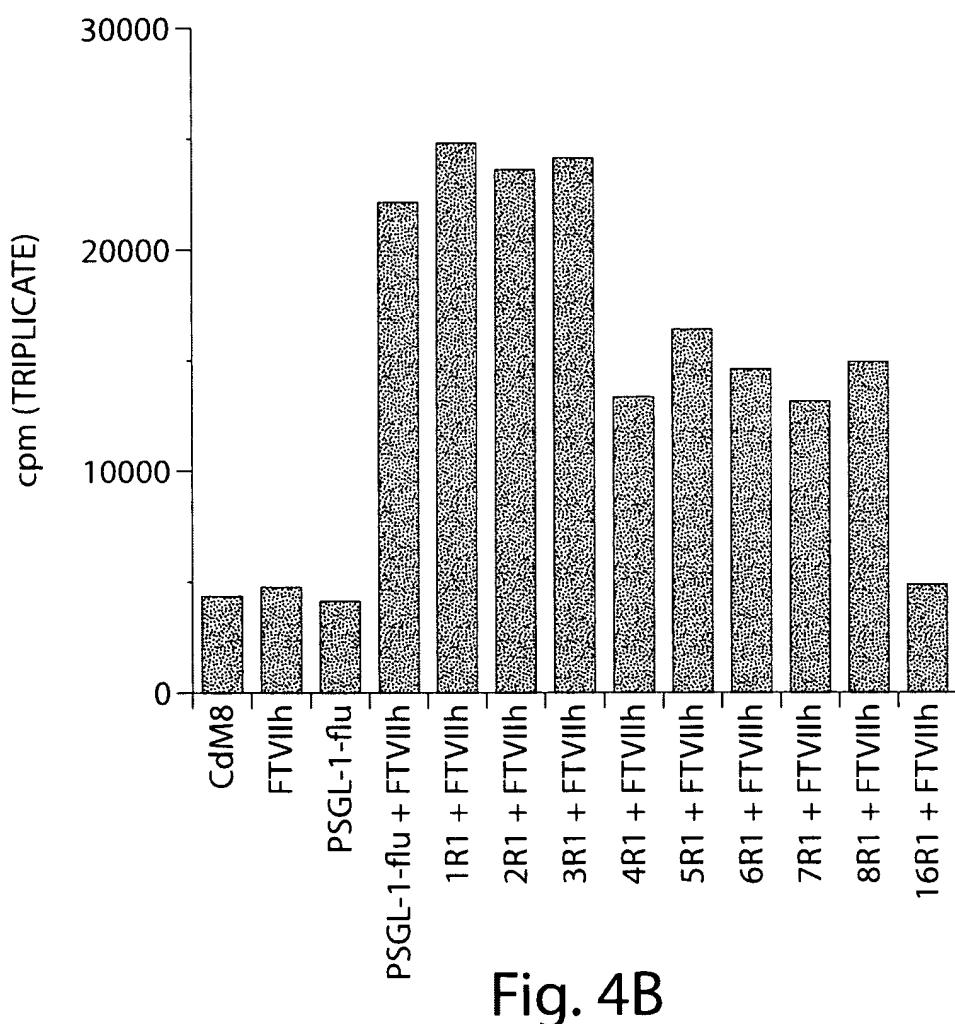


Fig. 3B





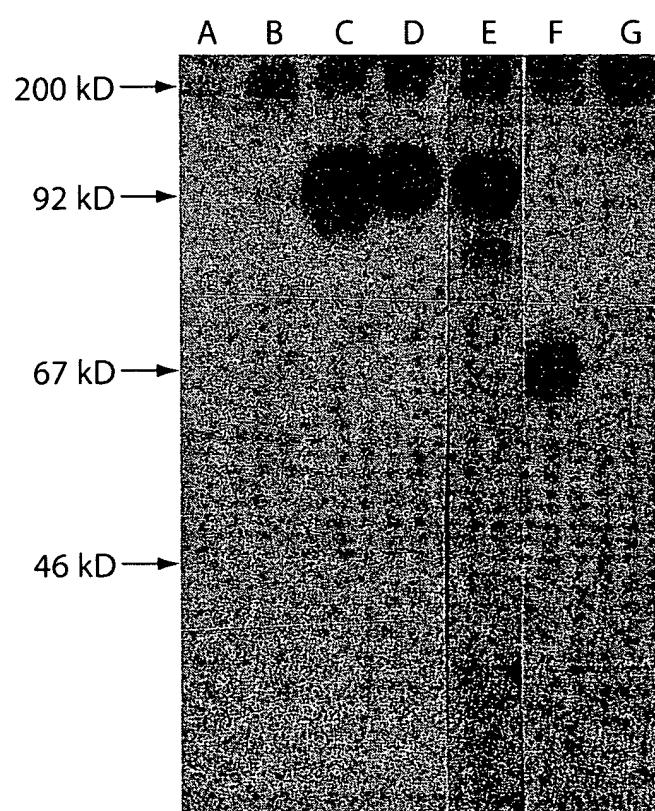


Fig. 5

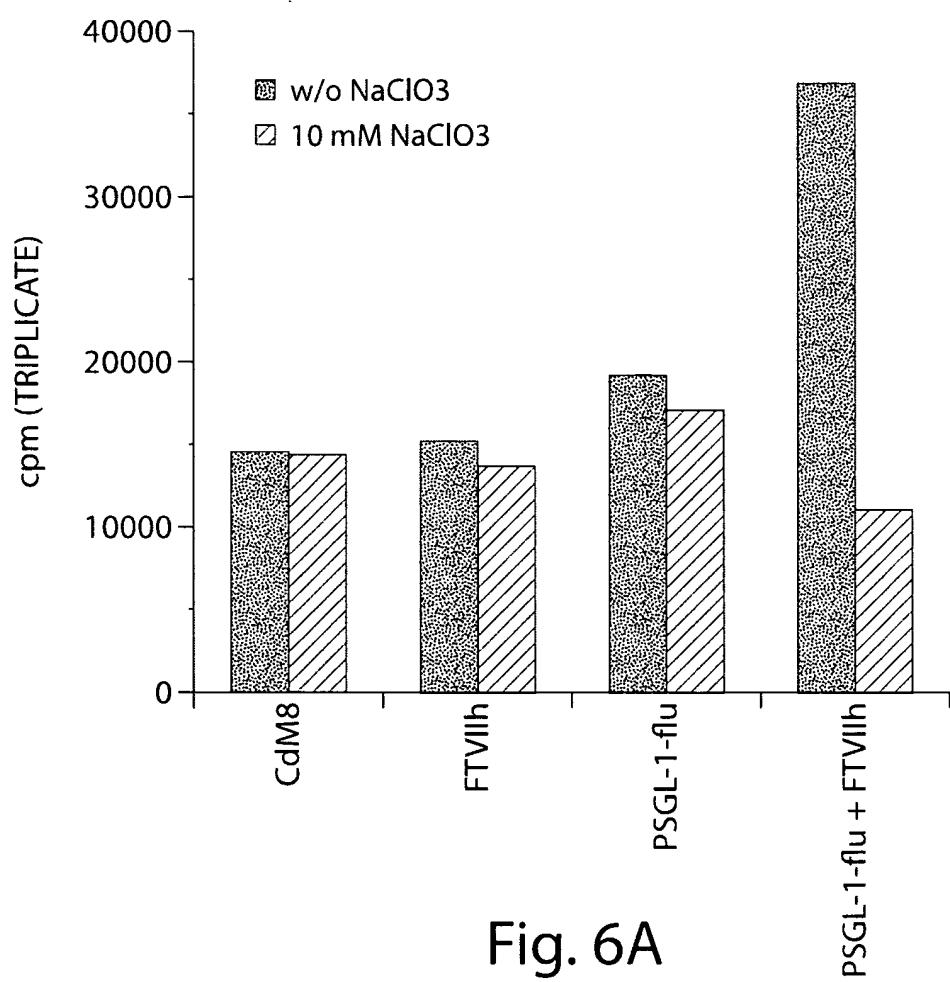
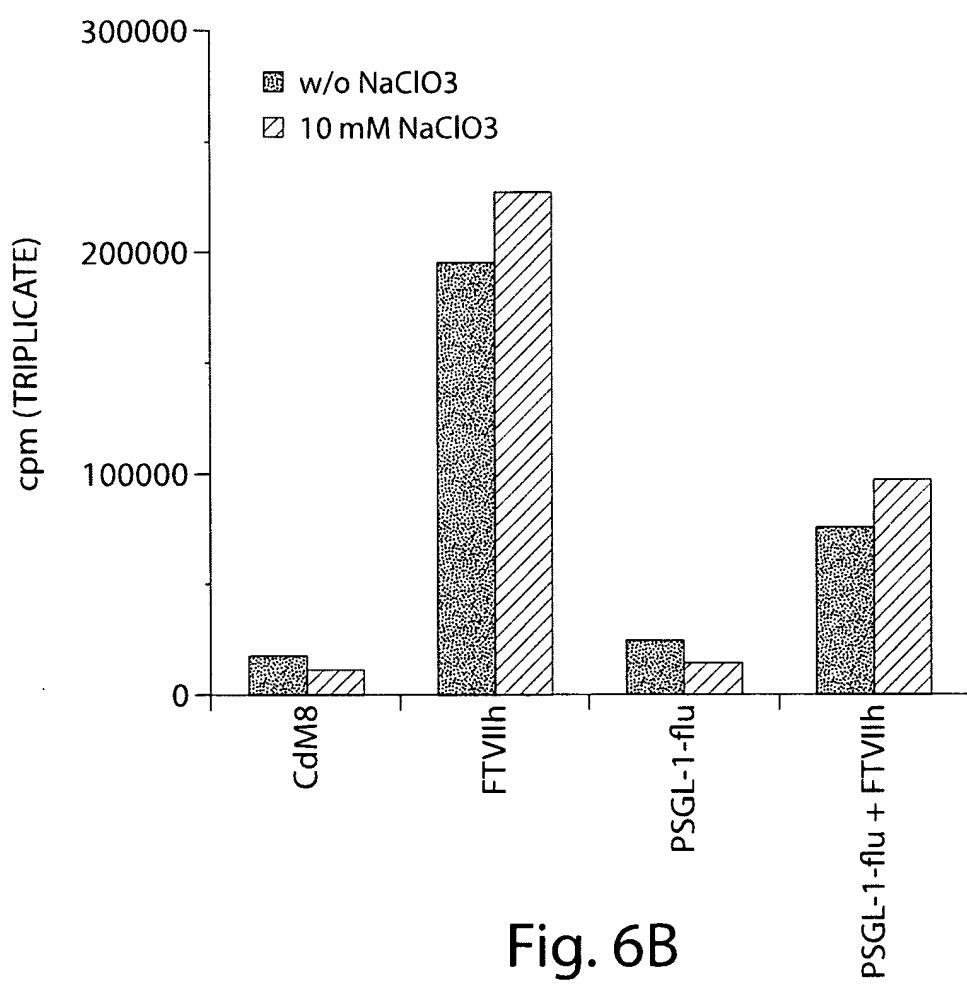


Fig. 6A



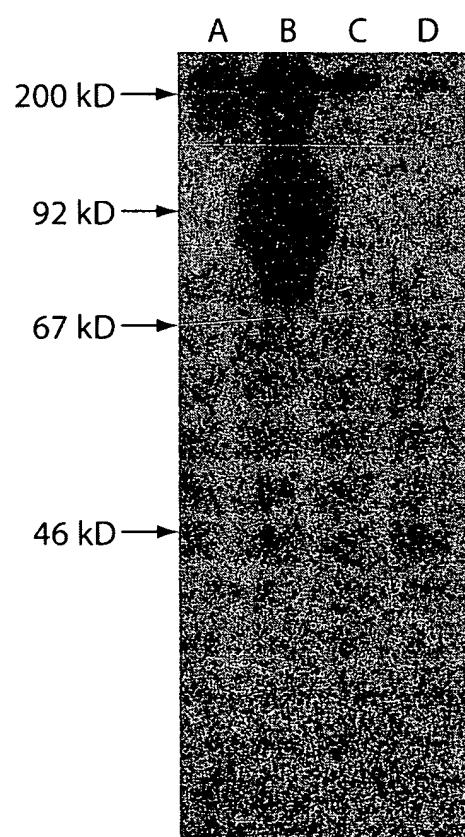


Fig. 7

Q19 R38 E58
 QLWDTWADEAEKALGPLLARDRRQATEYEYLDYDFLPETEPP
 P78 A98
 PEMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTE
 A108
 LTTELANMGNLSTD
 SA

Fig. 8A

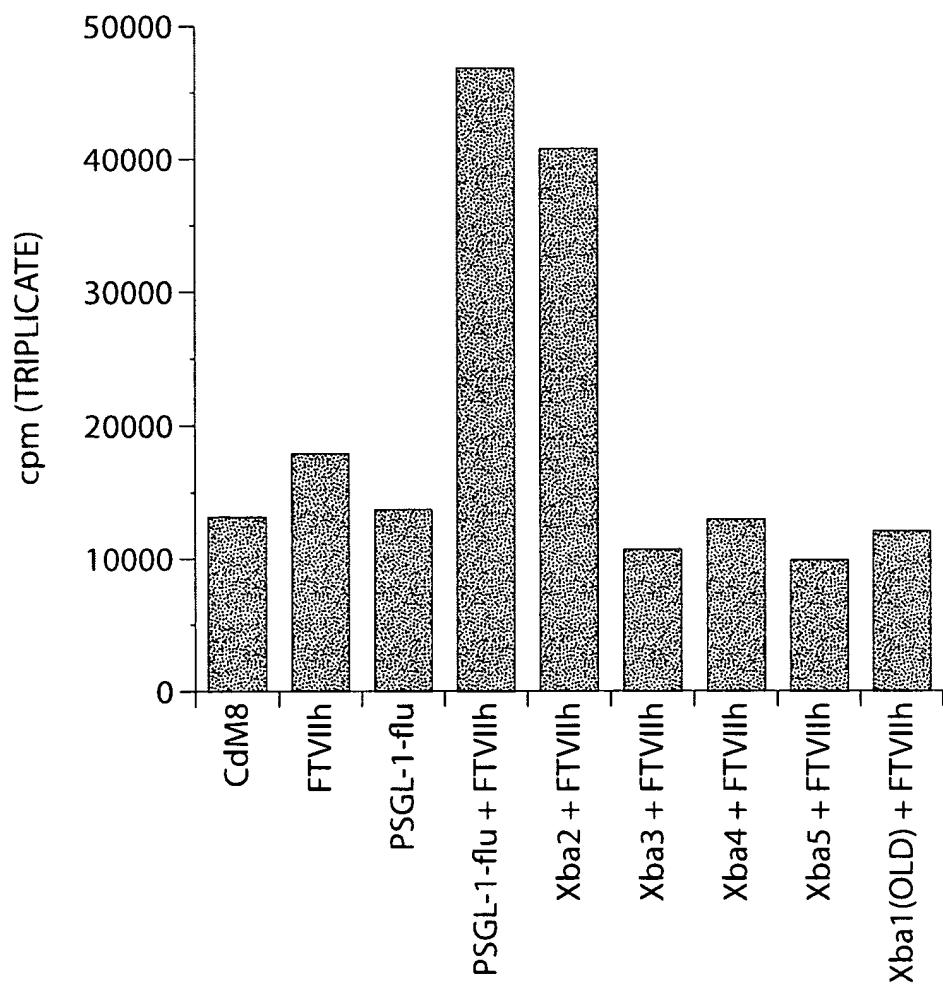


Fig. 8B

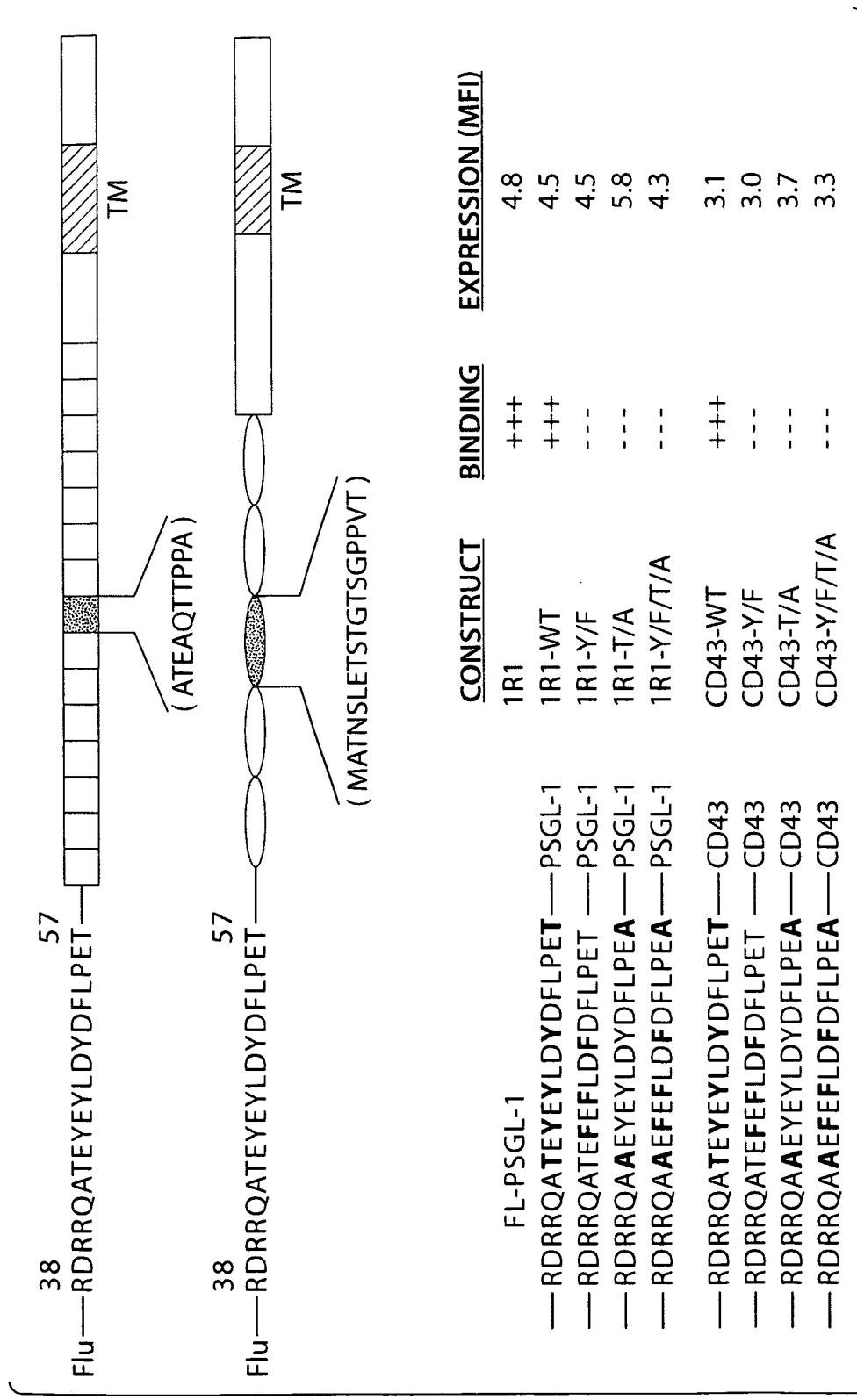


Fig. 9A

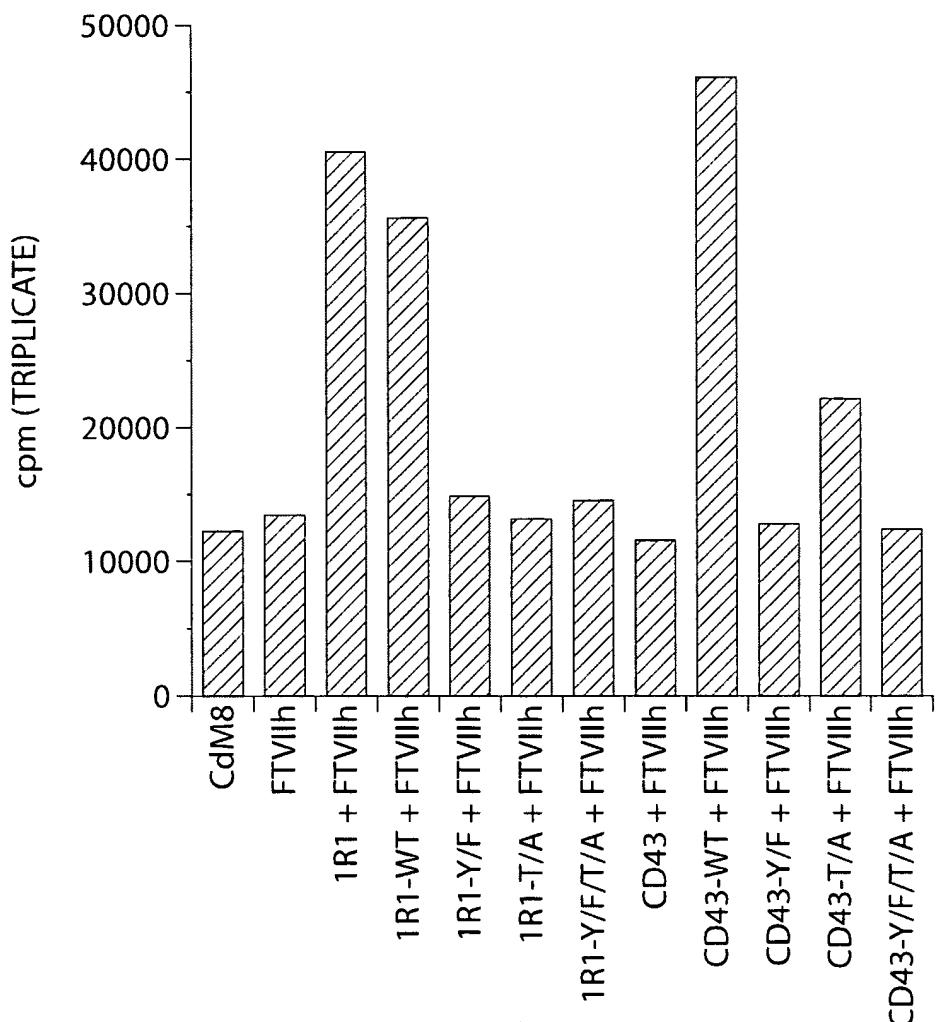


Fig. 9B

AAGCTTACCAACCATGGACTGGACCTGGAGGTTCTCTTGTGGTGGCAGCAGCTACA
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 TTCGAATGGTGGTACCTGACCTGGACCTCCAAGGAGAAGAACACCACCGTCGTCGATGT
 K L T T M D W T W R F L F F V V A A A T -

 GGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGTCC
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 CCACAGGTCAAGGGTCCACGTCGACCACGTCAGACCCGACTCCACTTCTCGGACCCAGG
 G V Q S Q V Q L V Q S G A E V K K P G S -

 TCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTCAGCAGCTATGCTATCAGCTGG
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 AGCCACTTCCAGAGGACGTTCCGAAGACCTCCGTGGAAGTCGTCGATACGATAGTCGACC
 S V K V S C K A S G G T F S S Y A I S W -

 GTGCGACAGGCCCTGGACAAGGGTTGAGTGGATGGAGGGATCATCCCTATCTTG
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 CACGCTGTCGGGGACCTGTTCCGAACTCACCTACCCCTCCCTAGTAGGGATAGAAACCA
 V R Q A P G Q G L E W M G G I I P I F G +

 ACAGCAAAC TACGCCACAGAACAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TGTCGTTGATGCGTGTCTCAAGGTCCGTCTCAGTGCTAATGGCGCCTGCTTAGGTGC
 T A N Y A Q K F Q G R V T I T A D E S T -

 AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 TCGTGTGGATGTACCTCGACTCGTCCGACTCTAGACTCCTGTGCCCCACATAATGACA
 S T A Y M E L S S L R S E D T A V Y Y C -

 GCGAGAGATAATGGAGCGTATTGTAGTGGTAGCTGCTACTCGGGCTGGTCGACCC
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 CGCTCTCTATTACCTCGCATAACATCACCACCATCGACGATGAGCCGACCAAGCTGGGG
 A R D N G A Y C S G G S C Y S G W F D P -

 TGGGGCCAGGGAACCTGGTACCGTCTCTCAGGTGAGTACTGAATTCTAGCTTCTGG
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 ACCCCGGTCCCTGGGACCAAGTGGCAGAGAAGTCCACTCATGACTTAAGATCGAAAGACC
 W G Q G T L V T V S S

Fig. 10A

GGCAGGCCAGGCCTGACCTGGCTTGGGGCAGGGAGGGGCTAAGGTGAGGCAGGTGGC
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 CCGTCCGGTCCGGACTGGAACCGAACCCCCGTCCCTCCCCGATTCCACTCCGTCCACCG

GCCAGCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCTGAACCTCGCGGAC
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 CGGTCTGCCACGTGTGGTTACGGGTACTCGGGTCTGTGACCTGCGACTTGGAGCGCCTG

AGTTAAGAACCCAGGGGCCTCTGCGCCTGGGCCAGCTCTGTCCCACACCGCGGTACAT
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 TCAATTCTGGGTCCCCGGAGACGCGGACCCGGGTCGAGACAGGGTGTGGCGCCAGTGTA

GGCACCACCTCTTGCAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCC
 661 -----+-----+-----+-----+-----+-----+-----+ 720
 CCGTGGTGGAGAGAACGTCGGAGGTGGTCCGGTAGCCAGAAGGGGGACCGTGGGAGG

A S T K G P S V F P L A P S -
 TCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCC
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 AGGTTCTCGTGGAGACCCCGTGTGCCGGGACCCGACGGACCAGTCCTGATGAAGGGG

S K S T S G G T A A L G C L V K D Y F P -
 GAACCGGTGACGGTGTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCG
 781 -----+-----+-----+-----+-----+-----+-----+ 840
 CTTGGCCACTGCCACAGCACCTTGAGTCCGGGACTGGTCGCCACGTGTGGAAGGGC

E P V T V S W N S G A L T S G V H T F P -
 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCCTCCAGC
 841 -----+-----+-----+-----+-----+-----+-----+ 900
 CGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTCGACCACTGGCACGGGAGGTG

A V L Q S S G L Y S L S S V V T V P S S -
 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATACAAGCCCAGCAACACCAAGGTG
 901 -----+-----+-----+-----+-----+-----+-----+ 960
 TCGAACCCGTGGTCTGGATGTAGACGTTGCACTTAGTGTGTTGGTCGTTGGTCCAC

S L G T Q T Y I C N V N H K P S N T K V -
 GACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAGCAGGCTC
 961 -----+-----+-----+-----+-----+-----+-----+ 1020
 CTGTTCTTCAACCACTCTCCGGTGTGTCCTCCACAGACGACCTCGTCCGAG

D K K V

Fig. 10B

1021 AGCGCTCCTGCCTGGACGCATCCCGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCAGGC
 TCGCGAGGACGGACCTGCGTAGGGCCGATACGTCGGGTCAAGTCCCCTCGTTCCGTCCG 1080

1081 CCCGTCTGCCTCTTCACCCGGAGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCT
 GGGCAGACGGAGAAGTGGGCCTCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGA 1140

1141 TCTGGCTTTTCCCAGGCTCTGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGC
 AGACCGAAAAAGGGTCCGAGACCCGTCCGTCCGATCCACGGGATTGGGTCCGGGACG 1200

1201 ACACAAAGGGCAGGTGCTGGCTCAGACCTGCCAAGAGCCATATCCGGGAGGACCTGC
 TGTGTTCCCGTCCACGACCCGAGTCTGGACGGTTCTCGGTATAGGCCCTCTGGGACG 1260

1261 CCCTGACCTAAGCCCACCCAAAGGCCAAACTCTCCACTCCCTCAGCTCGGACACCTCT
 GGGACTGGATTGGGTGGGTTCCGGTTGAGAGGTGAGGGAGTCGAGCCTGTGGAAGA 1320

1321 CTCCTCCCAGATTCCAGTAACTCCAATCTCTCTGCAGAGCCAAATCTTGACAA
 GAGGAGGGTCAAGGTATTGAGGGTTAGAAGAGAGACGTCTCGGGTTAGAACACTGTT 1380

E P K S C D K -

1381 AACTCACACATGCCACCGTGCCAGGTAAGCCAGGCCAGGCCTGCCCTCAGCTCAAG
 TTGAGTGTGTACGGTGGCACGGTCCATTGGTCCGGGAGCGGGAGGTGAGTT 1440

T H T C P P C P

1441 GCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCAGGCCGGTGCTGACA
 CGCCCTGTCCACGGATCTCATCGGACGTAGGTCCCTGTCCGGGTCGGCCACGACTGT 1500

1501 CGTCCACCTCCATCTCTCCTCAGCACCTGAACCTCTGGGGGACCGTCAGTCTCCTCT
 GCAGGTGGAGGTAGAGAAGGAGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGA 1560

A P E L L G G P S V F L F -

Fig. 10C

1561 TCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTGAGGTACATGCGTGG
 1620 AGGGGGTTTGGGTTCTGTGGAGTACTAGAGGCCTGGGACTCCAGTGTACGCACC
 P P K P K D T L M I S R T P E V T C V V -
 .
 1621 TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 1680 ACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACC
 N S
 V D V S H E D P E V K F N W Y V D G V E -
 .
 1681 AGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGG
 1740 TCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCCCACC
 N S
 V H N A K T K P R E E Q Y N S T Y R V V -
 .
 1741 TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGG
 1800 AGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCTCATGTTCACGTTCC
 N
 S V L T V L H Q D W L N G K E Y K C K V -
 .
 1801 TCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGA
 1860 AGAGGTTGTTCGGGAGGGTAGCTTTGGTAGAGGTTTCGGTTCCACCCCT
 N
 S N K A L P A P I E K T I S K A K
 .
 1861 CCCGTGGGTGCGAGGCCACATGGACAGAGGCCGGCTGGCCCACCCCTGAGA
 1920 GGGCACCCACGCTCCGGTGTACCTGTCTCCGGCGAGCCGGTAGACGGACTCT
 .
 1921 GTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACACAGGTGTACACCC
 1980 CACTGGCGACATGGTGGAGACAGGATGTCCCGTGGGCTTGGTGTCCACATGTGGG
 G Q P R E P Q V Y T L -
 .
 1981 TGCCCCCATCCGGGATGAGCTGACCAAGAACCAAGGTACGCTGACCTGCGTCAAAG
 2040 ACGGGGGTAGGGCCCTACTCGACTGGTTCTGGTCCAGTCGGACTGGACGGACCAAGTTTC
 P P S R D E L T K N Q V S L T C L V K G -

Fig. 10D

2041 GCTTCTATCCCAGCGACATGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACT
 CGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCTCGTTACCCGTCGGCCTTTGTTGA
 F Y P S D I A V E W E S N G Q P E N N Y -

 2101 ACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTCTTCCTACAGCAAGCTCA
 TGTTCTGGTGC GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGT
 K T T P P V L D S D G S F F L Y S K L T -

 2161 CCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTATGCATGAGG
 GGCACCTGTTCTCGTCCACCCTCGTCCCCTGCAGAAGAGTACGAGGCACTACGTACTCC
 V D K S R W Q Q G N V F S C S V M H E A -

 2221 CTCTGCACAACCACTACACGCAGAACAGAGCCTCTCCCTGTCTCCGGTAAATGAGTGCAC
 GAGACGTGTTGGTGATGTGGTCTTCTCGGAGAGGGACAGAGGCCATTACTCACGCTG
 L H N H Y T Q K S L S L S P G K *

 2281 GGCCGGC
 CCGGCCG

Fig. 10E

1 ATGGCGCTGT CCTGGGTTCT TACAGTCCTG AGCCTCCTAC CTCTGCTGGA
 51 AGCCCAGATC CCATTGTGTG CCAACCTAGT ACCGGTGCCC ATCACCAACG
 101 CCACCCTGGA CCAGATCACT GGCAAGTGGT TTTATATCGC ATCGGCCTTT
 151 CGAAACGAGG AGTACAATAA GTCGGTTTAG GAGATCCAAG CAACCTTCTT
 201 TTACTTCACC CCCAACAAAGA CAGAGGACAC GATCTTCTC AGAGAGTACC
 251 AGACCCGACA GGACCAGTGC ATCTATAACA CCACCTACCT GAATGTCCAG
 301 CGGGAAAATG GGACCATCTC CAGATACGTG GGAGGCCAAG AGCATTGCG
 351 TCACTTGCTG ATCCTCAGGG ACACCAAGAC CTACATGCTT GCTTTGACG
 401 TGAACGATGA GAAGAACTGG GGGCTGTCTG TCTATGCTGA CAAGCCAGAG
 451 ACGACCAAGG AGCAACTGGG AGAGTTCTAC GAAGCTCTCG ACTGCTTGC
 501 CATTCCCAAG TCAGATGTG TGTAACACCGA TTGGAAAAAG GATAAGTGTG
 551 AGCCACTGGA GAAGCAGCAC GAGAAGGAGA GGAAACAGGA GGAGGGGGAA
 601 TCGGATCCCG AGGGTGAGTA CTAAGCTTCA GCGCTCCTGC CTGGACGCAT
 651 CCCGGCTATG CAGCCCCAGT CCAGGGCAGC AAGGCAGGCC CCGTCTGCCT
 701 CTTCACCCGG AGCCTCTGCC CGCCCCACTC ATGCTCAGGG AGAGGGTCTT
 751 CTGGCTTTT CCCAGGCTCT GGGCAGGCAC AGGCTAGGTG CCCCTAACCC
 801 AGGCCCTGCA CACAAAGGGG CAGGTGCTGG GCTCAGACCT GCCAAGAGCC
 851 ATATCCGGGA GGACCTGCC CCTGACCTAA GCCCACCCCA AAGGCCAAC
 901 TCTCCACTCC CTCAGCTCGG ACACCTTCTC TCCTCCCAGA TTCCAGTAAC
 951 TCCCAATCTT CTCTCTGCAG AGCCCAAATC TTGTGACAAA ACTCACACAT
 1001 GCCCACCGTG CCCAGGTAAG CCAGCCCAGG CCTCGCCCTC CAGCTCAAGG
 1051 CGGGACAGGT GCCCTAGAGT AGCCTGCATC CAGGGACAGG CCCCAGCCGG
 1101 GTGCTGACAC GTCCACCTCC ATCTCTTCC CAGCACCTGA ACTCCTGGGG
 1151 GGACCGTCAG TCTTCCTCTT CCCCCCAAAA CCCAAGGACA CCCTCATGAT

22/26

1201 CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCCACGAAG
1251 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCCTGGA GGTGCATAAT
1301 GCCAAGACAA AGCCGCGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT
1351 CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAATGGC AAGGAGTACA
1401 AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA GAAAACCATC
1451 TCCAAAGCCA AAGGTGGGAC CCGTGGGTG CGAGGGCCAC ATGGACAGAG
1501 GCCGGCTCGG CCCACCCCTCT GCCCTGAGAG TGACCGCTGT ACCAACCTCT
1551 GTCCTACAGG GCAGCCCCGA GAACCACAGG TGTACACCCT GCCCCCCATCC
1601 CGGGATGAGC TGACCAAGAA CCAGGTCAGC CTGACCTGCC TGGTCAAAGG
1651 CTTCTATCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT GGGCAGCCGG
1701 AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA CGGCTCCTTC
1751 TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGAA
1801 CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC
1851 AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GAGTGCACG GCCG

Fig. 11B

1 M ALSWVLTVL SLLPLLEAQI PLCANLVPVP ITNATLDQIT GKWFYIASAF
51 RNEEYNKSVQ EIQTFFYFT PNKTEDTIFL REYQTRQDQC IYNTTYLNVQ
101 RENGTISRYV GGQEFAHLL ILRDTKYML AFDVNDEKNW GLSVYADKPE
151 TTKEQLGEFY EALDCLRIPK SDVVYTDWKK DKCEPLEKQH EKERQEEGE
201 SDPEGEPKSC DKTHCPPCP AP ELLGGPSV FLFPPKPKDT LMISRTPEVT
251 CVVVDVSHE D PEVKFNWYVD GVEVHN AAKTK PREEQYNSTY RVVSVLTVLH
301 QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK
351 NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTPPVVLDS DGSFFLYSKL
401 TVDKSRWQOG NVFSCSVMHE ALHNHYTQKS LSLSPGK*

Fig. 11C



Fig. 12A

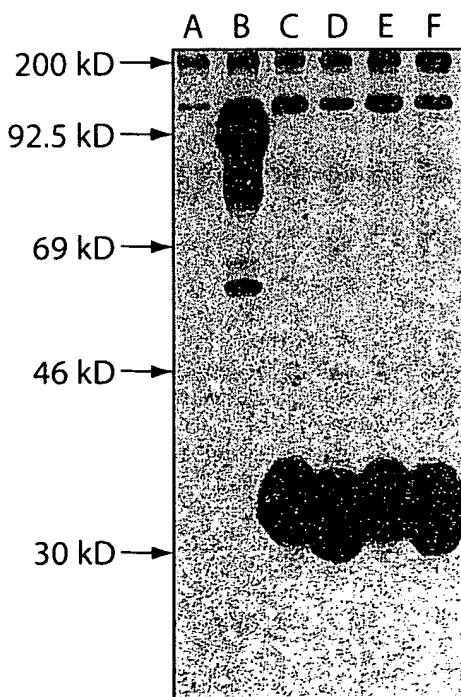


Fig. 12B

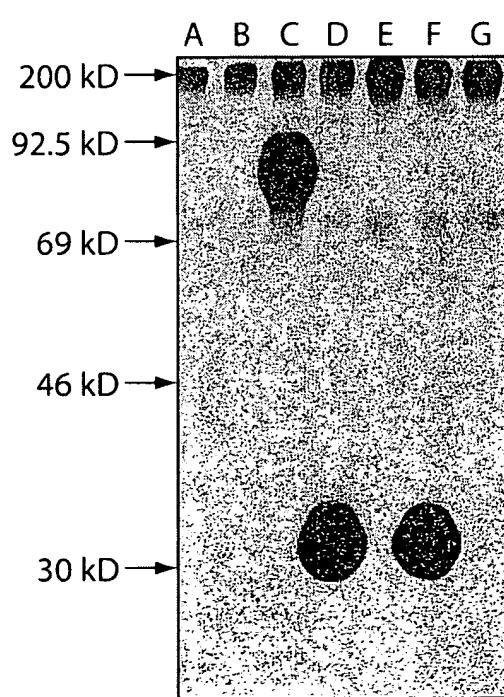


Fig. 12C

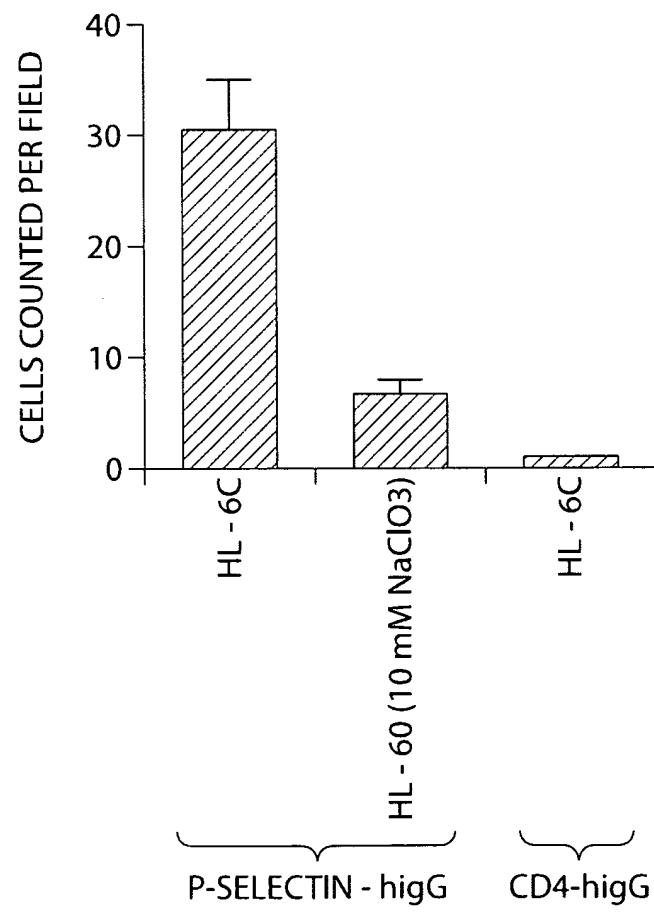


Fig. 13

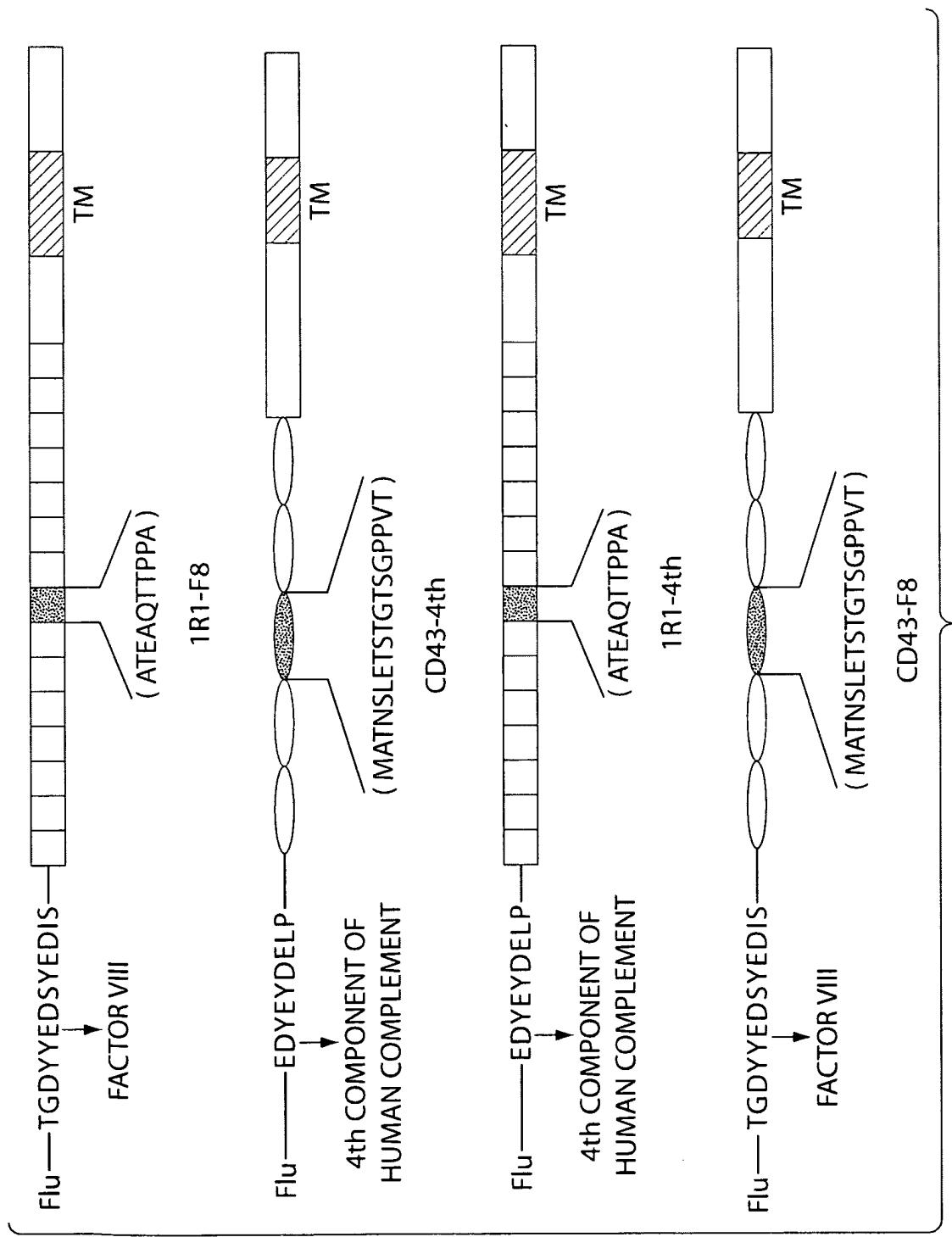


Fig. 14

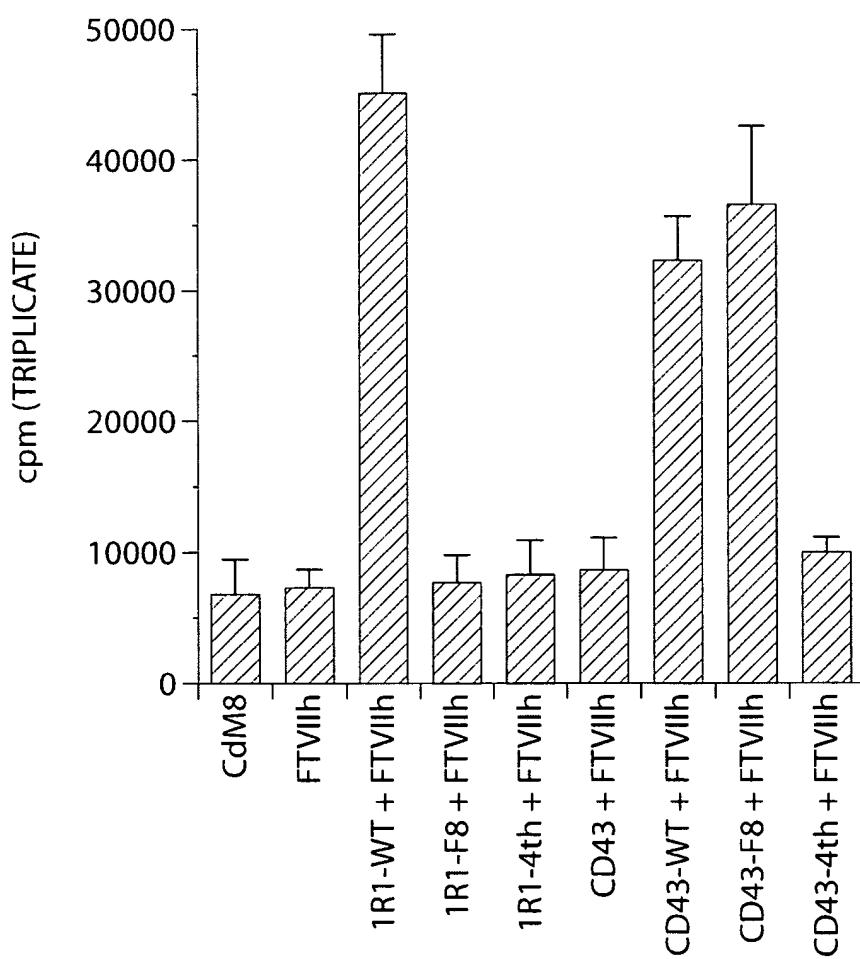


Fig. 15